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SEQUENCE LISTING

<110> Saleh, Mazen T.

Alexander, David C.

Liu, Jun

<120> Secreted Acid Phosphatase (sapM) is Present Only in Pathogenic Mycobacteria and Expressed Selectively at Phagosomal pH

<130> 4146 0005

<140>

<141>

<150> US 60/416,957

<151> 2002-10-09

<160> 22

<170> PatentIn version 3.0

<210> 1

<211> 500

<212> DNA

<213> Mycobacterium tuberculosis

<400> 1

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cggcaaggcg gcatgcgctt cgtcgacccat ccccaacccc gcccgcaaca caggaaagcag	180
caggggtggc ttggttagcc gcgacccgac cgtctcggcc agcggcgtag ggatcgggac	240
tggctcgcag ggcgcatcgc ggggtggcctc atagatcaac agcagcgtga gctcgcgcag	300
cgtgcccccg aagccggcgt tgcggtgcg ttcgtcacgc agcgtggtca gtcgggccgc	360
ggccagtggg tggtaacga catggacctg cagggcggtg aacctatat aacaatcgtg	420
gctcgggtccc ctaaaagggg gctgatacgg gtgcgtccat ccgcgcgacc ggtcaacccc	480
gtccatatac tcccggcatg	500

<210> 2

<211> 500

<212> DNA

<213> *Mycobacterium bovis*

<400> 2

catcgggtca agcaccatga ccggtacatc cgtcaggctc tccggcagcg agtccagata	60
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cggcaaggcg gcatgcgcct cgtcgaccat cccaacccc gcccgcaaca caggaaccag	180
caggggtggc ttggttagcc gcgacccgac cgtctcggcc agcggcgtag ggatcgggac	240
tggctcgcag ggcgcatcgc ggggtggcctc atagatcaac agcagcgtga gctcgcgcag	300
cgtgccccg aagccggcgt tgcgggtgcg ttcgtcacgc agcgtggtca gtcgggccgc	360
ggccagtggg tggtaacga catggacctg caccggcttg aacctatat aacaatcgtg	420
gctcgggtccc ctaaaagggg gctgatacgg gtgcgtccat ccgcgcgacc ggtcaacccc	480
gtccatatac tcccgcatg	500

<210> 3

<211> 500

<212> DNA

<213> *Mycobacterium avium*

<400> 3

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cggcgccaaa tacgggaccg gccgggtgggt ttgctcgtcg cgggcgacgc cgacgaagcc	120
cacctcggcc tcgggcagcg cggcctgcgc cgggtcgacc atgccagcc cggcgcgtag	180
caccggaacc agcagcggcg gattgaccag tcgggtcccg gcggccgcgg ccaccgggggt	240
gcggatccgg accgacttgc gcggcgcgtc gcggctggcc tcgtagacca gcatcagcgt	300
cagatcgcgc agcgcggccc gaaatccggc ggtgtcgggt cgttcgtcgc gcagcaccgt	360
cagccggggc gcggccaacg ggtggtcgat caccgacacg tccatctggt cgagggtata	420
taacgatcgg gcaaagcccc gctgacacgc ttgcccgccg gccggaaacg ccttaccgcc	480
gttcgtatac tccgggctg	500

<210> 4

<211> 500

<212> DNA

<213> *Mycobacterium marinum*

<400> 4
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 cgacccgcgc ctccggcagc gccgcatgcg ctctcgtcgac catgcccagt ccggcgcgca 180
 gcaccggaac cagaagcggg gggttggcca gtcttaggcc tgcgtggcc gcaagcggtg 240
 tacggatagc gacggattcg gtggcgctg cgcgggtcgc etcatagacc agtaccagtg 300
 tcagctcacg caaggccttg cggaaagcag cgtttccggg gcgttcgtca cgcagcggg 360
 tcaggcgggc cgccgccagc gggatgatcaa tgacgtggac ttccacatgg gtgaccctat 420
 ataacaatcg gattcaagcc gctgacacgc tccccctcct cgcggcgccg aggccgagcc 480
 gcccatatac tccgggctg 500

<210> 5
 <211> 43
 <212> PRT
 <213> Mycobacterium tuberculosis

<400> 5
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 Arg Ala Leu Ala Val Ile Gly Val Leu Ala Ala Ser Leu Leu Ala Ser
 20 25 30
 Trp Val Gly Ala Val Pro Gln Val Gly Leu Ala
 35 40

<210> 6
 <211> 43
 <212> PRT
 <213> Mycobacterium bovis

<400> 6
 Met Leu Arg Gly Ile Gln Ala Leu Ser Arg Pro Leu Thr Arg Val Tyr
 1 5 10 15
 Arg Ala Leu Ala Val Ile Gly Val Leu Ala Ala Ser Leu Leu Ala Ser
 20 25 30
 Trp Val Gly Ala Val Pro Gln Val Gly Leu Ala
 35 40

<210> 7
 <211> 42
 <212> PRT

<213> Mycobacterium avium

<400> 7

Met Ser Arg Glu Asn Arg Ser Arg Arg Arg Leu Ile Gly Gly Ala Tyr
1 5 10 15
Arg Ser Leu Arg Leu Leu Gly Ala Val Ala Ala Val Ala Leu Ala Ala
20 25 30
Ser Pro Leu Thr Pro Arg Thr Ser Leu Ala
35 40

<210> 8

<211> 40

<212> PRT

<213> Mycobacterium marinum

<400> 8

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Val Leu Gly Ala Val Ala Val Ser Leu Pro Ala His Gly Ser Asp Ala
20 25 30
Pro Pro Arg Ile Asp Leu Thr Ala
35 40

<210> 9

<211> 900

<212> DNA

<213> Mycobacterium tuberculosis

<220>

<221> CDS

<222> (1)..(900)

<400> 9

atg ctc cgc gga atc cag gct ctc agc cgg ccc ctg acc agg gta tac 48
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cgt gcc ttg gcg gtg atc ggt gtc ctg gca gca tcg ttg ctg gcc tca 96
Arg Ala Leu Ala Val Ile Gly Val Leu Ala Ala Ser Leu Leu Ala Ser
20 25 30
tgg gtc ggc gct gtc cca caa gtg ggt ctg gca gcg agt gcc ctg ccg 144
Trp Val Gly Ala Val Pro Gln Val Gly Leu Ala Ala Ser Ala Leu Pro
35 40 45
acc ttc gcg cac gtg gtc atc gtg gtg gag gag aac cgc tcg cag gcc 192

Thr	Phe	Ala	His	Val	Val	Ile	Val	Val	Glu	Glu	Asn	Arg	Ser	Gln	Ala		
50						55					60						
gcc atc atc ggt aac aag tcg gct ccc ttc atc aat tcg ctg gcc gcc	240																
Ala Ile Ile Gly Asn Lys Ser Ala Pro Phe Ile Asn Ser Leu Ala Ala																	
65 70 75 80																	
aac ggc gcg atg atg gcc cag gcg ttc gcc gaa aca cac ccg agc gaa	288																
Asn Gly Ala Met Met Ala Gln Ala Phe Ala Glu Thr His Pro Ser Glu																	
85 90 95																	
ccg aac tac ctg gca ctg ttc gct ggc aac aca ttc ggg ttg acg aag	336																
Pro Asn Tyr Leu Ala Leu Phe Ala Gly Asn Thr Phe Gly Leu Thr Lys																	
100 105 110																	
aac acc tgc ccc gtc aac ggc ggc gcg ctg ccc aac ctg ggt tct gag	384																
Asn Thr Cys Pro Val Asn Gly Gly Ala Leu Pro Asn Leu Gly Ser Glu																	
115 120 125																	
ttg ctc agc gcc ggt tac aca ttc atg ggg ttc gcc gaa gac ttg cct	432																
Leu Leu Ser Ala Gly Tyr Thr Phe Met Gly Phe Ala Glu Asp Leu Pro																	
130 135 140																	
gcg gtc ggc tcc acg gtg tgc agt gcg ggc aaa tac gca cgc aaa cac	480																
Ala Val Gly Ser Thr Val Cys Ser Ala Gly Lys Tyr Ala Arg Lys His																	
145 150 155 160																	
gtg ccg tgg gtc aac ttc agt aac gtg ccg acg aca ctg tcg gtg ccg	528																
Val Pro Trp Val Asn Phe Ser Asn Val Pro Thr Thr Leu Ser Val Pro																	
165 170 175																	
ttt tcg gca ttt ccg aag ccg cag aat tac ccc ggc ctg ccg acg gtg	576																
Phe Ser Ala Phe Pro Lys Pro Gln Asn Tyr Pro Gly Leu Pro Thr Val																	
180 185 190																	
tcg ttt gtc atc cct aac gcc gac aac gac atg cac gac ggc tcg atc	624																
Ser Phe Val Ile Pro Asn Ala Asp Asn Asp Met His Asp Gly Ser Ile																	
195 200 205																	
gcc caa ggc gac gcc tgg ctg aac cgc cac ctg tcg gca tat gcc aac	672																
Ala Gln Gly Asp Ala Trp Leu Asn Arg His Leu Ser Ala Tyr Ala Asn																	
210 215 220																	
tgg gcc aag aca aac aac agc ctg ctc gtt gtg acc tgg gac gaa gac	720																
Trp Ala Lys Thr Asn Asn Ser Leu Leu Val Val Thr Trp Asp Glu Asp																	
225 230 235 240																	
gac ggc agc agc cgc aat cag atc ccg acg gtg ttc tac ggc gcg cac	768																
Asp Gly Ser Ser Arg Asn Gln Ile Pro Thr Val Phe Tyr Gly Ala His																	
245 250 255																	
gtg cgg ccc gga act tac aac gag acc atc agc cac tac aac gtg ctg	816																
Val Arg Pro Gly Thr Tyr Asn Glu Thr Ile Ser His Tyr Asn Val Leu																	
260 265 270																	
tcc aca ttg gag cag atc tac gga ctg ccc aag acg ggt tat gcg acc	864																
Ser Thr Leu Glu Gln Ile Tyr Gly Leu Pro Lys Thr Gly Tyr Ala Thr																	
275 280 285																	
aat gct ccg cca ata acc gat att tgg ggc gac tag	900																
Asn Ala Pro Pro Ile Thr Asp Ile Trp Gly Asp																	
290 295																	

<210> 10

<211> 299

<212> PRT

<213> Mycobacterium tuberculosis

<400> 10

Met Leu Arg Gly Ile Gln Ala Leu Ser Arg Pro Leu Thr Arg Val Tyr
 1 5 10 15

Arg Ala Leu Ala Val Ile Gly Val Leu Ala Ala Ser Leu Leu Ala Ser
 20 25 30

Trp Val Gly Ala Val Pro Gln Val Gly Leu Ala Ala Ser Ala Leu Pro
 35 40 45

Thr Phe Ala His Val Val Ile Val Val Glu Glu Asn Arg Ser Gln Ala
 50 55 60

Ala Ile Ile Gly Asn Lys Ser Ala Pro Phe Ile Asn Ser Leu Ala Ala
 65 70 75 80

Asn Gly Ala Met Met Ala Gln Ala Phe Ala Glu Thr His Pro Ser Glu
 85 90 95

Pro Asn Tyr Leu Ala Leu Phe Ala Gly Asn Thr Phe Gly Leu Thr Lys
 100 105 110

Asn Thr Cys Pro Val Asn Gly Gly Ala Leu Pro Asn Leu Gly Ser Glu
 115 120 125

Leu Leu Ser Ala Gly Tyr Thr Phe Met Gly Phe Ala Glu Asp Leu Pro
 130 135 140

Ala Val Gly Ser Thr Val Cys Ser Ala Gly Lys Tyr Ala Arg Lys His
 145 150 155 160

Val Pro Trp Val Asn Phe Ser Asn Val Pro Thr Thr Leu Ser Val Pro
 165 170 175

Phe Ser Ala Phe Pro Lys Pro Gln Asn Tyr Pro Gly Leu Pro Thr Val
 180 185 190

Ser Phe Val Ile Pro Asn Ala Asp Asn Asp Met His Asp Gly Ser Ile
 195 200 205

Ala Gln Gly Asp Ala Trp Leu Asn Arg His Leu Ser Ala Tyr Ala Asn
 210 215 220

Trp Ala Lys Thr Asn Asn Ser Leu Leu Val Val Thr Trp Asp Glu Asp
 225 230 235 240

Asp Gly Ser Ser Arg Asn Gln Ile Pro Thr Val Phe Tyr Gly Ala His
 245 250 255

Val Arg Pro Gly Thr Tyr Asn Glu Thr Ile Ser His Tyr Asn Val Leu
 260 265 270

Ser Thr Leu Glu Gln Ile Tyr Gly Leu Pro Lys Thr Gly Tyr Ala Thr
 275 280 285

Asn Ala Pro Pro Ile Thr Asp Ile Trp Gly Asp
 290 295

<210> 11

<211> 900

<212> DNA

<213> Mycobacterium bovis

<220>

<221> CDS

<222> (1)..(900)

<400> 11

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cgt gcc ttg gcg gtg atc ggt gtc ctg gca gca tcg ttg ctg gcc tca 96
 Arg Ala Leu Ala Val Ile Gly Val Leu Ala Ala Ser Leu Ala Ser
 20 25 30

tgg gtc ggc gct gtc cca caa gtg ggt ctg gca gcg agt gcc ctg ccg 144
 Trp Val Gly Ala Val Pro Gln Val Gly Leu Ala Ala Ser Ala Leu Pro
 35 40 45

acc ttc gcg cac gtg gtc atc gtg gtg gag gag aac cgc tcg cag gcc 192
 Thr Phe Ala His Val Val Ile Val Val Glu Glu Asn Arg Ser Gln Ala
 50 55 60

gcc atc atc ggt aac aag tcg gct ccc ttc atc aat tcg ctg gcc gcc 240
 Ala Ile Ile Gly Asn Lys Ser Ala Pro Phe Ile Asn Ser Leu Ala Ala
 65 70 75 80

aac ggc gcg atg atg gcc cag gcg ttc gcc gaa aca cac ccg agc gaa 288
 Asn Gly Ala Met Met Ala Gln Ala Phe Ala Glu Thr His Pro Ser Glu
 85 90 95

ccg aac tac ctg gca ctg ttc gct ggc aac aca ttc ggg ttg acg aag 336
 Pro Asn Tyr Leu Ala Leu Phe Ala Gly Asn Thr Phe Gly Leu Thr Lys
 100 105 110

aac acc tgc ccc gtc aac ggc ggc gcg ctg ccc aac ctg ggt tct gag 384
 Asn Thr Cys Pro Val Asn Gly Gly Ala Leu Pro Asn Leu Gly Ser Glu
 115 120 125

ttg ctc agc gcc ggt tac aca ttc atg ggg ttc gcc gaa gac ttg cct 432

Leu Leu Ser Ala Gly Tyr Thr Phe Met Gly Phe Ala Glu Asp Leu Pro
 130 135 140
 gcg gtc ggc tcc acg gtg tgc agt gcg ggc aaa tac gca cgc aaa cac 480
 Ala Val Gly Ser Thr Val Cys Ser Ala Gly Lys Tyr Ala Arg Lys His
 145 150 155 160
 gtg ccg tgg gtc aac ttc agt aac gtg ccg gcg aca ctg tcg gtg ccg 528
 Val Pro Trp Val Asn Phe Ser Asn Val Pro Ala Thr Leu Ser Val Pro
 165 170 175
 ttt tcg gca ttt ccg aag ccg cag aat tac ccc ggc ctg ccg acg gtg 576
 Phe Ser Ala Phe Pro Lys Pro Gln Asn Tyr Pro Gly Leu Pro Thr Val
 180 185 190
 tcg ttt gtc atc cct aac gcc gac aac gac atg cac gac ggc tcg atc 624
 Ser Phe Val Ile Pro Asn Ala Asp Asn Asp Met His Asp Gly Ser Ile
 195 200 205
 gcc caa ggc gac gcc tgg ctg aac cgc cac ctg tcg gca tat gcc aac 672
 Ala Gln Gly Asp Ala Trp Leu Asn Arg His Leu Ser Ala Tyr Ala Asn
 210 215 220
 tgg gcc aag aca aac aac agc ctg ctc gtt gtg acc tgg gac gaa gac 720
 Trp Ala Lys Thr Asn Asn Ser Leu Leu Val Val Thr Trp Asp Glu Asp
 225 230 235 240
 gac ggc agc agc cgc aat cag atc ccg acg gtg ttc tac ggc gcg cac 768
 Asp Gly Ser Ser Arg Asn Gln Ile Pro Thr Val Phe Tyr Gly Ala His
 245 250 255
 gtg cgg ccc gga act tac aac gag acc atc agc cac tac aac gtg ctg 816
 Val Arg Pro Gly Thr Tyr Asn Glu Thr Ile Ser His Tyr Asn Val Leu
 260 265 270
 tcc aca ttg gag cag atc tac gga ctg ccc aag acg ggt tat gcg acc 864
 Ser Thr Leu Glu Gln Ile Tyr Gly Leu Pro Lys Thr Gly Tyr Ala Thr
 275 280 285
 aat gct ccg cca ata acc gat att tgg ggc gac tag 900
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 290 295

<210> 12

<211> 299

<212> PRT

<213> Mycobacterium bovis

<400> 12

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 1 5 10 15
 Arg Ala Leu Ala Val Ile Gly Val Leu Ala Ala Ser Leu Leu Ala Ser
 20 25 30
 Trp Val Gly Ala Val Pro Gln Val Gly Leu Ala Ala Ser Ala Leu Pro
 35 40 45

Thr Phe Ala His Val Val Ile Val Val Glu Glu Asn Arg Ser Gln Ala
50 55 60

Ala Ile Ile Gly Asn Lys Ser Ala Pro Phe Ile Asn Ser Leu Ala Ala
65 70 75 80

Asn Gly Ala Met Met Ala Gln Ala Phe Ala Glu Thr His Pro Ser Glu
85 90 95

Pro Asn Tyr Leu Ala Leu Phe Ala Gly Asn Thr Phe Gly Leu Thr Lys
100 105 110

Asn Thr Cys Pro Val Asn Gly Gly Ala Leu Pro Asn Leu Gly Ser Glu
115 120 125

Leu Leu Ser Ala Gly Tyr Thr Phe Met Gly Phe Ala Glu Asp Leu Pro
130 135 140

Ala Val Gly Ser Thr Val Cys Ser Ala Gly Lys Tyr Ala Arg Lys His
145 150 155 160

Val Pro Trp Val Asn Phe Ser Asn Val Pro Ala Thr Leu Ser Val Pro
165 170 175

Phe Ser Ala Phe Pro Lys Pro Gln Asn Tyr Pro Gly Leu Pro Thr Val
180 185 190

Ser Phe Val Ile Pro Asn Ala Asp Asn Asp Met His Asp Gly Ser Ile
195 200 205

Ala Gln Gly Asp Ala Trp Leu Asn Arg His Leu Ser Ala Tyr Ala Asn
210 215 220

Trp Ala Lys Thr Asn Asn Ser Leu Leu Val Val Thr Trp Asp Glu Asp
225 230 235 240

Asp Gly Ser Ser Arg Asn Gln Ile Pro Thr Val Phe Tyr Gly Ala His
245 250 255

Val Arg Pro Gly Thr Tyr Asn Glu Thr Ile Ser His Tyr Asn Val Leu
260 265 270

Ser Thr Leu Glu Gln Ile Tyr Gly Leu Pro Lys Thr Gly Tyr Ala Thr
275 280 285

Asn Ala Pro Pro Ile Thr Asp Ile Trp Gly Asp
290 295

<210> 13

<211> 903

<212> DNA

<213> Mycobacterium avium

<220>

<221> CDS

<222> (1)..(903)

<400> 13

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1			5						10					15		
cga	agc	ctg	cgg	ctg	ctc	ggc	gcc	gtg	gcc	gcg	gtg	gcg	ctg	gcg	gcc	96
Arg	Ser	Leu	Arg	Leu	Leu	Gly	Ala	Val	Ala	Ala	Val	Ala	Leu	Ala	Ala	
		20					25						30			
agc	ccg	ttg	aca	ccg	cgc	acc	agc	ctt	gcg	gca	gcg	gcc	att	ccg	caa	144
Ser	Pro	Leu	Thr	Pro	Arg	Thr	Ser	Leu	Ala	Ala	Ala	Ala	Ile	Pro	Gln	
		35					40					45				
ccg	tcg	cac	atc	gtg	atc	gtg	gtg	gag	gaa	aac	cgt	tcc	gag	agc	ggc	192
Pro	Ser	His	Ile	Val	Ile	Val	Val	Glu	Glu	Asn	Arg	Ser	Glu	Ser	Gly	
		50				55					60					
atc	atc	ggc	aac	aag	tcg	gcg	ccc	ttc	atc	acc	gcg	ctg	gcc	gcg	tcc	240
Ile	Ile	Gly	Asn	Lys	Ser	Ala	Pro	Phe	Ile	Thr	Ala	Leu	Ala	Ala	Ser	
65					70				75					80		
ggc	gcc	aac	atg	acc	cag	tcg	ttc	gcc	gaa	acc	cac	ccc	agc	gag	ccc	288
Gly	Ala	Asn	Met	Thr	Gln	Ser	Phe	Ala	Glu	Thr	His	Pro	Ser	Glu	Pro	
			85						90					95		
aat	tac	ctg	gcg	ctg	ttc	gcc	ggc	aac	acg	ttc	ggg	gtg	acc	aag	gac	336
Asn	Tyr	Leu	Ala	Leu	Phe	Ala	Gly	Asn	Thr	Phe	Gly	Val	Thr	Lys	Asp	
		100					105						110			
ctg	tgc	ccg	gtc	aac	gcc	ggc	gcc	gca	ccc	aac	ctg	ggg	tcc	gaa	ttg	384
Leu	Cys	Pro	Val	Asn	Ala	Gly	Ala	Ala	Pro	Asn	Leu	Gly	Ser	Glu	Leu	
		115					120					125				
ctc	gcc	gcc	ggt	tac	aca	ttc	gcc	ggc	tac	gcc	gag	ggc	ctg	ccg	tcc	432
Leu	Ala	Ala	Gly	Tyr	Thr	Phe	Ala	Gly	Tyr	Ala	Glu	Gly	Leu	Pro	Ser	
		130				135					140					
ccg	ggc	tca	ccg	gtg	tgc	agt	gcg	ggc	aag	tac	gcg	cga	aaa	cat	gtg	480
Pro	Gly	Ser	Pro	Val	Cys	Ser	Ala	Gly	Lys	Tyr	Ala	Arg	Lys	His	Val	
145					150				155					160		
ccg	tgg	gcc	aac	ttc	acc	aac	gtg	ccg	gcg	gcg	agc	tcg	ctg	ccg	ttc	528
Pro	Trp	Ala	Asn	Phe	Thr	Asn	Val	Pro	Ala	Ala	Ser	Ser	Leu	Pro	Phe	
			165						170					175		
tcg	gcg	ttc	ccg	atg	ggc	aac	tac	gcc	agc	ctg	ccg	acg	gtg	tcg	ttc	576
Ser	Ala	Phe	Pro	Met	Gly	Asn	Tyr	Ala	Ser	Leu	Pro	Thr	Val	Ser	Phe	
			180				185						190			
gtc	atc	ccg	aac	aac	gac	aac	aac	atg	cac	gac	ggc	tcg	atc	gcg	cag	624
Val	Ile	Pro	Asn	Asn	Asp	Asn	Asn	Met	His	Asp	Gly	Ser	Ile	Ala	Gln	
		195					200					205				
gcc	gac	gcc	tgg	ctg	aac	cgg	cag	ctg	tcc	ggc	tac	gcc	aat	tgg	gcg	672

Ala Asp Ala Trp Leu Asn Arg Gln Leu Ser Gly Tyr Ala Asn Trp Ala
 210 215 220

ctg gcc aac aac agc ctg ctg atc gtc acc ttc gac gag gac gac aac 720
 Leu Ala Asn Asn Ser Leu Leu Ile Val Thr Phe Asp Glu Asp Asp Asn
 225 230 235 240

tcc aac gtc gga gcc agc cgc aac cag atc ccc acg gtg ttc tac ggc 768
 Ser Asn Val Gly Ala Ser Arg Asn Gln Ile Pro Thr Val Phe Tyr Gly
 245 250 255

gcc cac gtc cgc ccc ggc aac tac gcc gag cag atc aac cac tac aac 816
 Ala His Val Arg Pro Gly Asn Tyr Ala Glu Gln Ile Asn His Tyr Asn
 260 265 270

gtg ctt gcc acc ctc gag cag atg tac ggg ctg ccc aag acg ggc tat 864
 Val Leu Ala Thr Leu Glu Gln Met Tyr Gly Leu Pro Lys Thr Gly Tyr
 275 280 285

gcc gcc ggc gcc gcc ccc atc acc gac atc tgg ggc tga 903
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 290 295 300

<210> 14

<211> 300

<212> PRT

<213> Mycobacterium avium

<400> 14

Met Ser Arg Glu Asn Arg Ser Arg Arg Arg Leu Ile Gly Gly Ala Tyr
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Arg Ser Leu Arg Leu Leu Gly Ala Val Ala Ala Val Ala Leu Ala Ala
 20 25 30

Ser Pro Leu Thr Pro Arg Thr Ser Leu Ala Ala Ala Ala Ile Pro Gln
 35 40 45

Pro Ser His Ile Val Ile Val Val Glu Glu Asn Arg Ser Glu Ser Gly
 50 55 60

Ile Ile Gly Asn Lys Ser Ala Pro Phe Ile Thr Ala Leu Ala Ala Ser
 65 70 75 80

Gly Ala Asn Met Thr Gln Ser Phe Ala Glu Thr His Pro Ser Glu Pro
 85 90 95

Asn Tyr Leu Ala Leu Phe Ala Gly Asn Thr Phe Gly Val Thr Lys Asp
 100 105 110

Leu Cys Pro Val Asn Ala Gly Ala Ala Pro Asn Leu Gly Ser Glu Leu
 115 120 125

Leu Ala Ala Gly Tyr Thr Phe Ala Gly Tyr Ala Glu Gly Leu Pro Ser
130 135 140

Pro Gly Ser Pro Val Cys Ser Ala Gly Lys Tyr Ala Arg Lys His Val
145 150 155 160

Pro Trp Ala Asn Phe Thr Asn Val Pro Ala Ala Ser Ser Leu Pro Phe
165 170 175

Ser Ala Phe Pro Met Gly Asn Tyr Ala Ser Leu Pro Thr Val Ser Phe
180 185 190

Val Ile Pro Asn Asn Asp Asn Asn Met His Asp Gly Ser Ile Ala Gln
195 200 205

Ala Asp Ala Trp Leu Asn Arg Gln Leu Ser Gly Tyr Ala Asn Trp Ala
210 215 220

Leu Ala Asn Asn Ser Leu Leu Ile Val Thr Phe Asp Glu Asp Asp Asn
225 230 235 240

Ser Asn Val Gly Ala Ser Arg Asn Gln Ile Pro Thr Val Phe Tyr Gly
245 250 255

Ala His Val Arg Pro Gly Asn Tyr Ala Glu Gln Ile Asn His Tyr Asn
260 265 270

Val Leu Ala Thr Leu Glu Gln Met Tyr Gly Leu Pro Lys Thr Gly Tyr
275 280 285

Ala Ala Gly Ala Ala Pro Ile Thr Asp Ile Trp Gly
290 295 300

<210> 15

<211> 888

<212> DNA

<213> Mycobacterium marinum

<220>

<221> CDS

<222> (1)..(888)

<400> 15

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1 5 10 15

gta ctc ggc gcg gtg gcg gta tcc cta ccg gcc cac ggt agc gac gct 96

Val	Leu	Gly	Ala	Val	Ala	Val	Ser	Leu	Pro	Ala	His	Gly	Ser	Asp	Ala	
			20					25					30			
ccc	ccg	cgt	atc	gac	ctg	acc	gcc	act	gcg	ttg	ccg	gcg	ttc	tca	cat	144
Pro	Pro	Arg	Ile	Asp	Leu	Thr	Ala	Thr	Ala	Leu	Pro	Ala	Phe	Ser	His	
		35					40					45				
gtg	gtg	gtc	gtg	gtg	gag	gag	aac	cat	tcg	cag	gcc	aac	atc	att	ggc	192
Val	Val	Val	Val	Val	Glu	Glu	Asn	His	Ser	Gln	Ala	Asn	Ile	Ile	Gly	
	50					55					60					
aac	aag	gcg	gcc	ccg	ttc	atc	aat	gcg	ctg	gcc	gcc	aac	ggc	gcg	atg	240
Asn	Lys	Ala	Ala	Pro	Phe	Ile	Asn	Ala	Leu	Ala	Ala	Asn	Gly	Ala	Met	
65				70					75					80		
atg	tcg	cag	tcg	ttc	gcc	gaa	acg	cac	ccc	agc	gaa	ccc	aac	tac	ctg	288
Met	Ser	Gln	Ser	Phe	Ala	Glu	Thr	His	Pro	Ser	Glu	Pro	Asn	Tyr	Leu	
			85						90					95		
gcc	ttg	ttc	gcc	ggc	acc	acc	ttc	ggc	ttg	aag	aag	aac	acg	tgt	ccg	336
Ala	Leu	Phe	Ala	Gly	Thr	Thr	Phe	Gly	Leu	Lys	Lys	Asn	Thr	Cys	Pro	
			100					105					110			
gtc	aat	gcg	ggc	agc	acg	ccc	aac	ctg	gct	tcg	gag	ttg	ctc	gcc	gcg	384
Val	Asn	Ala	Gly	Ser	Thr	Pro	Asn	Leu	Ala	Ser	Glu	Leu	Leu	Ala	Ala	
		115					120					125				
ggc	cac	acg	ttc	gta	ggc	ttc	gcc	gag	agc	ctg	ccc	gaa	gtc	ggc	tcg	432
Gly	His	Thr	Phe	Val	Gly	Phe	Ala	Glu	Ser	Leu	Pro	Glu	Val	Gly	Ser	
	130					135					140					
acg	gtc	tgc	agc	gcc	gga	aag	tac	ggg	cgc	aag	cat	gcg	cct	tgg	gtg	480
Thr	Val	Cys	Ser	Ala	Gly	Lys	Tyr	Gly	Arg	Lys	His	Ala	Pro	Trp	Val	
145					150				155					160		
aac	ttc	agc	aat	gtt	ccg	gcc	acg	ctg	tcg	atg	ccc	ttc	tcc	gcg	ttt	528
Asn	Phe	Ser	Asn	Val	Pro	Ala	Thr	Leu	Ser	Met	Pro	Phe	Ser	Ala	Phe	
				165					170					175		
ccg	acg	ccg	gcg	gac	tac	gcc	agg	ctg	ccc	acg	gtg	tcc	ttc	gtc	atc	576
Pro	Thr	Pro	Ala	Asp	Tyr	Ala	Arg	Leu	Pro	Thr	Val	Ser	Phe	Val	Ile	
			180					185					190			
ccc	aac	ggg	gat	aac	aac	atg	cac	gac	ggc	acc	atc	gcg	gca	gct	gac	624
Pro	Asn	Gly	Asp	Asn	Asn	Met	His	Asp	Gly	Thr	Ile	Ala	Ala	Ala	Asp	
		195				200						205				
gag	tgg	ttg	aac	cgt	caa	ctg	tcg	ccg	tac	gcc	aac	tgg	gcc	cga	tcc	672
Glu	Trp	Leu	Asn	Arg	Gln	Leu	Ser	Pro	Tyr	Ala	Asn	Trp	Ala	Arg	Ser	
	210					215						220				
aac	aac	agc	ctg	ctg	atc	gtg	acg	tgg	gat	gag	gac	gac	ggc	ggc	agc	720
Asn	Asn	Ser	Leu	Leu	Ile	Val	Thr	Trp	Asp	Glu	Asp	Asp	Gly	Gly	Ser	
225					230					235				240		
cgc	aac	cag	att	ccc	acg	gtg	ttc	tac	ggc	gca	cac	gta	cgg	ccg	ggc	768
Arg	Asn	Gln	Ile	Pro	Thr	Val	Phe	Tyr	Gly	Ala	His	Val	Arg	Pro	Gly	
				245					250					255		
act	tac	aac	cag	acc	atc	agc	cac	tac	aac	gtg	ctt	tcc	acg	ctg	gag	816
Thr	Tyr	Asn	Gln	Thr	Ile	Ser	His	Tyr	Asn	Val	Leu	Ser	Thr	Leu	Glu	
			260					265					270			
cag	atg	tac	ggc	ttg	ccc	aag	acg	ggc	ttc	gcg	gcg	aac	gcc	ccg	gtc	864
Gln	Met	Tyr	Gly	Leu	Pro	Lys	Thr	Gly	Phe	Ala	Ala	Ala	Ala	Pro	Val	
		275					280					285				
atc	gct	gat	atc	tgg	ggc	ggc	taa									888

Ile Ala Asp Ile Trp Gly Gly
290 295

<210> 16

<211> 295

<212> PRT

<213> Mycobacterium marinum

<400> 16

Met Cys Gly Leu Lys Gln Arg Phe Thr Ser Thr Phe Arg Ala Leu Ala
1 5 10 15

Val Leu Gly Ala Val Ala Val Ser Leu Pro Ala His Gly Ser Asp Ala
20 25 30

Pro Pro Arg Ile Asp Leu Thr Ala Thr Ala Leu Pro Ala Phe Ser His
35 40 45

Val Val Val Val Val Glu Glu Asn His Ser Gln Ala Asn Ile Ile Gly
50 55 60

Asn Lys Ala Ala Pro Phe Ile Asn Ala Leu Ala Ala Asn Gly Ala Met
65 70 75 80

Met Ser Gln Ser Phe Ala Glu Thr His Pro Ser Glu Pro Asn Tyr Leu
85 90 95

Ala Leu Phe Ala Gly Thr Thr Phe Gly Leu Lys Lys Asn Thr Cys Pro
100 105 110

Val Asn Ala Gly Ser Thr Pro Asn Leu Ala Ser Glu Leu Leu Ala Ala
115 120 125

Gly His Thr Phe Val Gly Phe Ala Glu Ser Leu Pro Glu Val Gly Ser
130 135 140

Thr Val Cys Ser Ala Gly Lys Tyr Gly Arg Lys His Ala Pro Trp Val
145 150 155 160

Asn Phe Ser Asn Val Pro Ala Thr Leu Ser Met Pro Phe Ser Ala Phe
165 170 175

Pro Thr Pro Ala Asp Tyr Ala Arg Leu Pro Thr Val Ser Phe Val Ile
180 185 190

Pro Asn Gly Asp Asn Asn Met His Asp Gly Thr Ile Ala Ala Ala Asp
195 200 205

Glu Trp Leu Asn Arg Gln Leu Ser Pro Tyr Ala Asn Trp Ala Arg Ser
 210 215 220

Asn Asn Ser Leu Leu Ile Val Thr Trp Asp Glu Asp Asp Gly Gly Ser
 225 230 235 240

Arg Asn Gln Ile Pro Thr Val Phe Tyr Gly Ala His Val Arg Pro Gly
 245 250 255

Thr Tyr Asn Gln Thr Ile Ser His Tyr Asn Val Leu Ser Thr Leu Glu
 260 265 270

Gln Met Tyr Gly Leu Pro Lys Thr Gly Phe Ala Ala Asn Ala Pro Val
 275 280 285

Ile Ala Asp Ile Trp Gly Gly
 290 295

<210> 17

<211> 1291

<212> DNA

<213> *Penicillium chrysogenum*

<220>

<221> CDS

<222> (1) .. (213)

<220>

<221> intro

<222> (217) .. (244)

<220>

<221> CDS

<222> (245) .. (1288)

<400> 17
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 Met Leu Thr Lys Gln Thr Leu Leu Ala Phe Val Gly Ala Leu Ala Leu
 1 5 10 15

gcc acg ggt aca act acc act gaa gag acc cca act cag gct gag att 96
 Ala Thr Gly Thr Thr Thr Glu Glu Thr Pro Thr Gln Ala Glu Ile
 20 25 30

gat gca gca cgt gct acg gcc ctg cct tac tct cct gtg tca aac gta 144

Asp	Ala	Ala	Arg	Ala	Thr	Ala	Leu	Pro	Tyr	Ser	Pro	Val	Ser	Asn	Val		
	35						40					45					
aag	ggt	ttg	gcc	ttt	gat	cgt	ttc	gtg	aac	atc	tgg	ctc	gag	aac	aca		192
Lys	Gly	Leu	Ala	Phe	Asp	Arg	Phe	Val	Asn	Ile	Trp	Leu	Glu	Asn	Thr		
	50					55					60						
gta	ggt	ttc	ccg	ttg	aat	ata	taacaatgac	cacgcgctca	cccccttgta	g							244
Val	Gly	Phe	Pro	Leu	Asn	Ile											
	65					70											
gac	ttt	gaa	ccc	gct	gct	tta	gac	gag	aac	ctg	tcc	aag	ctg	gcc	aag		292
Asp	Phe	Glu	Pro	Ala	Ala	Leu	Asp	Glu	Asn	Leu	Ser	Lys	Leu	Ala	Lys		
			75					80					85				
gag	ggt	atc	ctc	ctg	acc	aac	tac	ttt	gcc	atc	tct	cac	ccc	tcg	cag		340
Glu	Gly	Ile	Leu	Leu	Thr	Asn	Tyr	Phe	Ala	Ile	Ser	His	Pro	Ser	Gln		
		90					95					100					
ccc	aac	tac	tgt	gct	tcc	gcc	ggg	ggt	gac	aca	ttc	ggc	atg	gat	aat		388
Pro	Asn	Tyr	Cys	Ala	Ser	Ala	Gly	Gly	Asp	Thr	Phe	Gly	Met	Asp	Asn		
	105					110					115						
gac	gac	ttc	cta	caa	atc	cct	tcg	aat	gtc	tca	act	att	gcc	gat	ctc		436
Asp	Asp	Phe	Leu	Gln	Ile	Pro	Ser	Asn	Val	Ser	Thr	Ile	Ala	Asp	Leu		
	120				125				130						135		
ttt	gat	act	aag	cac	atc	tct	tgg	ggt	gaa	tac	caa	gaa	gac	atg	ccc		484
Phe	Asp	Thr	Lys	His	Ile	Ser	Trp	Gly	Glu	Tyr	Gln	Glu	Asp	Met	Pro		
				140				145						150			
tat	gct	ggc	tac	caa	ggc	aaa	cgg	tat	ccc	ctc	agc	ggt	ccg	aac	cag		532
Tyr	Ala	Gly	Tyr	Gln	Gly	Lys	Arg	Tyr	Pro	Leu	Ser	Gly	Pro	Asn	Gln		
			155					160					165				
tac	gtg	cgc	aag	cac	aac	ccg	ctg	gtt	ttg	ttt	aac	tcg	gtt	acc	gac		580
Tyr	Val	Arg	Lys	His	Asn	Pro	Leu	Val	Leu	Phe	Asn	Ser	Val	Thr	Asp		
		170				175						180					
gac	gcc	gtg	cgc	ccg	cgc	caa	atc	aag	aat	ttc	acc	act	ttc	tac	gac		628
Asp	Ala	Val	Arg	Pro	Arg	Gln	Ile	Lys	Asn	Phe	Thr	Thr	Phe	Tyr	Asp		
	185					190					195						
gat	ctg	aag	cac	cac	agc	ctt	ccc	caa	cac	atg	ttc	atc	aca	ccg	aac		676
Asp	Leu	Lys	His	His	Ser	Leu	Pro	Gln	His	Met	Phe	Ile	Thr	Pro	Asn		
	200				205					210					215		
atg	acc	aat	gac	gcc	cac	gac	acg	aac	atc	act	gtg	gcc	ggt	aac	tgg		724
Met	Thr	Asn	Asp	Ala	His	Asp	Thr	Asn	Ile	Thr	Val	Ala	Gly	Asn	Trp		
				220				225						230			
gtc	gat	cgc	ttc	ctg	tct	cct	cta	ctg	aag	aac	gag	tac	ttc	acc	aag		772
Val	Asp	Arg	Phe	Leu	Ser	Pro	Leu	Leu	Lys	Asn	Glu	Tyr	Phe	Thr	Lys		
			235					240					245				
gac	agc	cta	gtg	cta	ctc	acc	ttt	gac	gag	gga	gac	acc	tac	tcc	tac		820
Asp	Ser	Leu	Val	Leu	Leu	Thr	Phe	Asp	Glu	Gly	Asp	Thr	Tyr	Ser	Tyr		
		250					255					260					
ccc	aac	cgg	gtc	ttc	agc	ttc	ctt	gtt	gga	ggt	gct	atc	cca	gag	cac		868
Pro	Asn	Arg	Val	Phe	Ser	Phe	Leu	Val	Gly	Gly	Ala	Ile	Pro	Glu	His		
	265					270						275					
ctg	aag	ggg	acc	act	gac	gac	act	ttc	tac	acc	cac	tac	tca	att	gtc		916
Leu	Lys	Gly	Thr	Thr	Asp	Thr	Phe	Tyr	Thr	His	Tyr	Ser	Ile	Val			
	280				285			290						295			
gct	tcc	ctg	tct	gct	aac	tgg	ggt	tta	ccc	tcg	ctt	ggt	cgc	tgg	gat		964

Ala Ser Leu Ser Ala Asn Trp Gly Leu Pro Ser Leu Gly Arg Trp Asp
 300 305 310

tgt ggc gcc aac ctg ctg aag atg gtc gct gac aag acc ggc tat gtc 1012
 Cys Gly Ala Asn Leu Leu Lys Met Val Ala Asp Lys Thr Gly Tyr Val
 315 320 325

aac tgg gaa gtt gat acc agc aat gtc tac ctc aac gag act tac cct 1060
 Asn Trp Glu Val Asp Thr Ser Asn Val Tyr Leu Asn Glu Thr Tyr Pro
 330 335 340

gga cct atg tct acc gac aac tat tcc tct aag tgg gcc gtt cct gcc 1108
 Gly Pro Met Ser Thr Asp Asn Tyr Ser Ser Lys Trp Ala Val Pro Ala
 345 350 355

acc aag ggc aaa tgc tct gct ggc cat ggc att gct gag gtc gtg aag 1156
 Thr Lys Gly Lys Cys Ser Ala Gly His Gly Ile Ala Glu Val Val Lys
 360 365 370 375

aat acc tac cac ggg ctt caa ccc acc tac gac tat gcc agc cct gta 1204
 Asn Thr Tyr His Gly Leu Gln Pro Thr Tyr Asp Tyr Ala Ser Pro Val
 380 385 390

ccg tat gac gtg acc agt gga aac aac gtc ggc atc aag tac cac cgc 1252
 Pro Tyr Asp Val Thr Ser Gly Asn Asn Val Gly Ile Lys Tyr His Arg
 395 400 405

act ctg gta tgt atc ctt tca tgt tct tcc ctt tca tga 1291
 Thr Leu Val Cys Ile Leu Ser Cys Ser Ser Leu Ser
 410 415

<210> 18

<211> 71

<212> PRT

<213> Penicillium chrysogenum

<400> 18

Met Leu Thr Lys Gln Thr Leu Leu Ala Phe Val Gly Ala Leu Ala Leu
 1 5 10 15

Ala Thr Gly Thr Thr Thr Thr Glu Glu Thr Pro Thr Gln Ala Glu Ile
 20 25 30

Asp Ala Ala Arg Ala Thr Ala Leu Pro Tyr Ser Pro Val Ser Asn Val
 35 40 45

Lys Gly Leu Ala Phe Asp Arg Phe Val Asn Ile Trp Leu Glu Asn Thr
 50 55 60

Val Gly Phe Pro Leu Asn Ile
 65 70

<210> 19

<211> 348

<212> PRT

<213> Penicillium chrysogenum

<400> 19

Asp Phe Glu Pro Ala Ala Leu Asp Glu Asn Leu Ser Lys Leu Ala Lys
 1 5 10 15

Glu Gly Ile Leu Leu Thr Asn Tyr Phe Ala Ile Ser His Pro Ser Gln
 20 25 30

Pro Asn Tyr Cys Ala Ser Ala Gly Gly Asp Thr Phe Gly Met Asp Asn
 35 40 45

Asp Asp Phe Leu Gln Ile Pro Ser Asn Val Ser Thr Ile Ala Asp Leu
 50 55 60

Phe Asp Thr Lys His Ile Ser Trp Gly Glu Tyr Gln Glu Asp Met Pro
 65 70 75 80

Tyr Ala Gly Tyr Gln Gly Lys Arg Tyr Pro Leu Ser Gly Pro Asn Gln
 85 90 95

Tyr Val Arg Lys His Asn Pro Leu Val Leu Phe Asn Ser Val Thr Asp
 100 105 110

Asp Ala Val Arg Pro Arg Gln Ile Lys Asn Phe Thr Thr Phe Tyr Asp
 115 120 125

Asp Leu Lys His His Ser Leu Pro Gln His Met Phe Ile Thr Pro Asn
 130 135 140

Met Thr Asn Asp Ala His Asp Thr Asn Ile Thr Val Ala Gly Asn Trp
 145 150 155 160

Val Asp Arg Phe Leu Ser Pro Leu Leu Lys Asn Glu Tyr Phe Thr Lys
 165 170 175

Asp Ser Leu Val Leu Leu Thr Phe Asp Glu Gly Asp Thr Tyr Ser Tyr
 180 185 190

Pro Asn Arg Val Phe Ser Phe Leu Val Gly Gly Ala Ile Pro Glu His
 195 200 205

Leu Lys Gly Thr Thr Asp Asp Thr Phe Tyr Thr His Tyr Ser Ile Val
 210 215 220

Ala Ser Leu Ser Ala Asn Trp Gly Leu Pro Ser Leu Gly Arg Trp Asp
 225 230 235 240

Cys Gly Ala Asn Leu Leu Lys Met Val Ala Asp Lys Thr Gly Tyr Val
245 250 255

Asn Trp Glu Val Asp Thr Ser Asn Val Tyr Leu Asn Glu Thr Tyr Pro
260 265 270

Gly Pro Met Ser Thr Asp Asn Tyr Ser Ser Lys Trp Ala Val Pro Ala
275 280 285

Thr Lys Gly Lys Cys Ser Ala Gly His Gly Ile Ala Glu Val Val Lys
290 295 300

Asn Thr Tyr His Gly Leu Gln Pro Thr Tyr Asp Tyr Ala Ser Pro Val
305 310 315 320

Pro Tyr Asp Val Thr Ser Gly Asn Asn Val Gly Ile Lys Tyr His Arg
325 330 335

Thr Leu Val Cys Ile Leu Ser Cys Ser Ser Leu Ser
340 345

<210> 20

<211> 1457

<212> DNA

<213> Aspergillus fumigatus

<220>

<221> CDS

<222> (1) .. (186)

<220>

<221> Intron

<222> (187) .. (239)

<220>

<221> CDS

<222> (240) .. (301)

<220>

<221> Intron

<222> (302) . . (361)

<220>

<221> CDS

<222> (362)..(1454)

<400> 20

atg aag cct tcc gtc gcg act ttg ctt gcc act gtc tct ctg gtc tat	48
Met Lys Pro Ser Val Ala Thr Leu Leu Ala Thr Val Ser Leu Val Tyr	
1 5 10 15	
gct cag act gct act gag aag gag cct tcg ctg tct gcg ata gaa tct	96
Ala Gln Thr Ala Thr Glu Lys Glu Pro Ser Leu Ser Ala Ile Glu Ser	
20 25 30	
gca gca gcc tcc atc cag cct tac tct ccc gtt tcg aac gtt gag ggt	144
Ala Ala Ala Ser Ile Gln Pro Tyr Ser Pro Val Ser Asn Val Glu Gly	
35 40 45	
gtt gca ttt aat cgc ttc ttc caa gtg tgg ctt gag aat att	186
Val Ala Phe Asn Arg Phe Phe Gln Val Trp Leu Glu Asn Ile	
50 55 60	
gtatgtgac accctaccaa tcagagaatc ttgttcaaag ctgacctcag aag gat	242
Asp	
tac gag gat gct gcg gcg gat gag aac atg aaa tgg ctg gcc tcg caa	290
Tyr Glu Asp Ala Ala Ala Asp Glu Asn Met Lys Trp Leu Ala Ser Gln	
65 70 75	
ggg atc ctg ct gtaagacctc atatcggccca tctgctcacg atttgaactt	341
Gly Ile Leu Leu	
80	
cgaactaatt tactccacag c acc aat ttc tat gca gtc acg cat cct tca	392
Thr Asn Phe Tyr Ala Val Thr His Pro Ser	
85 90	
gag cca aac tac tgc gct gct gtt gga ggc gac aca ttt ggc atg gac	440
Glu Pro Asn Tyr Cys Ala Ala Val Gly Gly Asp Thr Phe Gly Met Asp	
95 100 105	
aat gac aac ttt aac cag att cct gcc aat gtt tct act gtc gct gat	488
Asn Asp Asn Phe Asn Gln Ile Pro Ala Asn Val Ser Thr Val Ala Asp	
110 115 120 125	
ctc ctg gac acc aaa aac att gct tgg gga gag tat cag gag cac tta	536
Leu Leu Asp Thr Lys Asn Ile Ala Trp Gly Glu Tyr Gln Glu His Leu	
130 135 140	
cct tat ccc gga ttc caa ggt ttc aac tat tcc aac cag gag act tat	584
Pro Tyr Pro Gly Phe Gln Gly Phe Asn Tyr Ser Asn Gln Glu Thr Tyr	
145 150 155	
gtc aat gac tat gtg cgc aag cat aac cca ctg gtc ttg tat gac tct	632
Val Asn Asp Tyr Val Arg Lys His Asn Pro Leu Val Leu Tyr Asp Ser	
160 165 170	
gtc acc aag aac agc act cgt ttg cgc cag atc aag aac ttt acc agc	680
Val Thr Lys Asn Ser Thr Arg Leu Arg Gln Ile Lys Asn Phe Thr Ser	
175 180 185	
ttc gag gac gac ctg gcc aac aag aaa ctt cct caa tgg gca ttt atc	728

Phe	Glu	Asp	Asp	Leu	Ala	Asn	Lys	Lys	Leu	Pro	Gln	Trp	Ala	Phe	Ile		
190					195					200					205		
act	cca	aac	atg	acc	aac	gac	gct	cat	gac	acc	aac	att	act	ttc	gga		776
Thr	Pro	Asn	Met	Thr	Asn	Asp	Ala	His	Asp	Thr	Asn	Ile	Thr	Phe	Gly		
				210					215					220			
gcc	aaa	tgg	gag	cga	agc	tgg	att	gcg	ccc	ttg	ctc	aac	aac	tca	tac		824
Ala	Lys	Trp	Glu	Arg	Ser	Trp	Ile	Ala	Pro	Leu	Leu	Asn	Asn	Ser	Tyr		
			225					230					235				
ttc	atg	aat	gat	acc	cta	atc	cta	ctt	acc	ttt	gat	gag	gat	ggc	act		872
Phe	Met	Asn	Asp	Thr	Leu	Ile	Leu	Leu	Thr	Phe	Asp	Glu	Asp	Gly	Thr		
		240					245					250					
tat	tcc	aag	agc	aac	aag	atc	ttc	agt	gtt	ctt	ctc	ggg	ggg	gcc	att		920
Tyr	Ser	Lys	Ser	Asn	Lys	Ile	Phe	Ser	Val	Leu	Leu	Gly	Gly	Ala	Ile		
		255				260					265						
ccc	gat	gag	ctg	aag	ggg	act	cag	gac	gat	acg	ttc	tat	acc	cac	tac		968
Pro	Asp	Glu	Leu	Lys	Gly	Thr	Gln	Asp	Asp	Thr	Phe	Tyr	Thr	His	Tyr		
270					275					280					285		
tca	gtg	att	gcg	tcc	gtg	tcc	gcg	aac	tgg	ggc	ctt	cct	tcg	ttg	gga		1016
Ser	Val	Ile	Ala	Ser	Val	Ser	Ala	Asn	Trp	Gly	Leu	Pro	Ser	Leu	Gly		
				290					295					300			
agg	tgg	gat	tgt	ggg	gcg	aac	att	ctt	gag	att	gtg	gca	aac	aag	acg		1064
Arg	Trp	Asp	Cys	Gly	Ala	Asn	Ile	Leu	Glu	Ile	Val	Ala	Asn	Lys	Thr		
			305					310					315				
gga	tat	gtc	aac	tac	gac	gtt	gac	aca	acc	aat	ctc	cgc	ctc	aac	gag		1112
Gly	Tyr	Val	Asn	Tyr	Asp	Val	Asp	Thr	Thr	Asn	Leu	Arg	Leu	Asn	Glu		
		320					325					330					
acc	tac	ccc	ggg	ccc	atg	tca	gcg	ggc	gaa	tac	tcg	aaa	tac	tcc	cct		1160
Thr	Tyr	Pro	Gly	Pro	Met	Ser	Ala	Gly	Glu	Tyr	Ser	Lys	Tyr	Ser	Pro		
		335				340					345						
gtc	tgg	ccg	aat	gcc	ttg	acc	cgt	ggg	gac	tgc	tct	gct	ggc	cat	ggc		1208
Val	Trp	Pro	Asn	Ala	Leu	Thr	Arg	Gly	Asp	Cys	Ser	Ala	Gly	His	Gly		
350				355					360					365			
att	ttg	gac	att	gtc	aag	gag	acc	tac	gcc	aac	acg	gag	cca	aca	tac		1256
Ile	Leu	Asp	Ile	Val	Lys	Glu	Thr	Tyr	Ala	Asn	Thr	Glu	Pro	Thr	Tyr		
				370					375					380			
aac	tat	tcg	agc	ccc	ttc	cca	tat	gac	act	gcg	agc	aac	tac	aac	acc		1304
Asn	Tyr	Ser	Ser	Pro	Phe	Pro	Tyr	Asp	Thr	Ala	Ser	Asn	Tyr	Asn	Thr		
			385					390					395				
aag	gtg	act	gcc	acc	aaa	aag	aat	gtc	acc	ggg	aca	cat	aga	agt	tct		1352
Lys	Val	Thr	Ala	Thr	Lys	Lys	Asn	Val	Thr	Gly	Thr	His	Arg	Ser	Ser		
			400				405					410					
tct	tcc	tcc	tct	ccg	tca	gct	agc	tcc	aac	gcc	gct	gtt	tct	gct	gtc		1400
Ser	Ser	Ser	Ser	Pro	Ser	Ala	Ser	Ser	Asn	Ala	Ala	Val	Ser	Ala	Val		
			415			420				425							
gct	cct	gca	gcc	ggg	gtc	tct	ggg	ctc	ctc	ttg	gga	ctc	gct	cta	aac		1448
Ala	Pro	Ala	Ala	Gly	Val	Ser	Gly	Leu	Leu	Leu	Gly	Leu	Ala	Leu	Asn		
430					435					440				445			
ctg	ctt	taa															1457
Leu	Leu																

<210> 21

<211> 447

<212> PRT

<213> Aspergillus fumigatus

<400> 21

Met Lys Pro Ser Val Ala Thr Leu Leu Ala Thr Val Ser Leu Val Tyr
 1 5 10 15

Ala Gln Thr Ala Thr Glu Lys Glu Pro Ser Leu Ser Ala Ile Glu Ser
 20 25 30

Ala Ala Ala Ser Ile Gln Pro Tyr Ser Pro Val Ser Asn Val Glu Gly
 35 40 45

Val Ala Phe Asn Arg Phe Phe Gln Val Trp Leu Glu Asn Ile Asp Tyr
 50 55 60

Glu Asp Ala Ala Ala Asp Glu Asn Met Lys Trp Leu Ala Ser Gln Gly
 65 70 75 80

Ile Leu Leu Thr Asn Phe Tyr Ala Val Thr His Pro Ser Glu Pro Asn
 85 90 95

Tyr Cys Ala Ala Val Gly Gly Asp Thr Phe Gly Met Asp Asn Asp Asn
 100 105 110

Phe Asn Gln Ile Pro Ala Asn Val Ser Thr Val Ala Asp Leu Leu Asp
 115 120 125

Thr Lys Asn Ile Ala Trp Gly Glu Tyr Gln Glu His Leu Pro Tyr Pro
 130 135 140

Gly Phe Gln Gly Phe Asn Tyr Ser Asn Gln Glu Thr Tyr Val Asn Asp
 145 150 155 160

Tyr Val Arg Lys His Asn Pro Leu Val Leu Tyr Asp Ser Val Thr Lys
 165 170 175

Asn Ser Thr Arg Leu Arg Gln Ile Lys Asn Phe Thr Ser Phe Glu Asp
 180 185 190

Asp Leu Ala Asn Lys Lys Leu Pro Gln Trp Ala Phe Ile Thr Pro Asn
 195 200 205

Met Thr Asn Asp Ala His Asp Thr Asn Ile Thr Phe Gly Ala Lys Trp
 210 215 220

Glu Arg Ser Trp Ile Ala Pro Leu Leu Asn Asn Ser Tyr Phe Met Asn
 225 230 235 240

Asp Thr Leu Ile Leu Leu Thr Phe Asp Glu Asp Gly Thr Tyr Ser Lys
 245 250 255

Ser Asn Lys Ile Phe Ser Val Leu Leu Gly Gly Ala Ile Pro Asp Glu
 260 265 270

Leu Lys Gly Thr Gln Asp Asp Thr Phe Tyr Thr His Tyr Ser Val Ile
 275 280 285

Ala Ser Val Ser Ala Asn Trp Gly Leu Pro Ser Leu Gly Arg Trp Asp
 290 295 300

Cys Gly Ala Asn Ile Leu Glu Ile Val Ala Asn Lys Thr Gly Tyr Val
 305 310 315 320

Asn Tyr Asp Val Asp Thr Thr Asn Leu Arg Leu Asn Glu Thr Tyr Pro
 325 330 335

Gly Pro Met Ser Ala Gly Glu Tyr Ser Lys Tyr Ser Pro Val Trp Pro
 340 345 350

Asn Ala Leu Thr Arg Gly Asp Cys Ser Ala Gly His Gly Ile Leu Asp
 355 360 365

Ile Val Lys Glu Thr Tyr Ala Asn Thr Glu Pro Thr Tyr Asn Tyr Ser
 370 375 380

Ser Pro Phe Pro Tyr Asp Thr Ala Ser Asn Tyr Asn Thr Lys Val Thr
 385 390 395 400

Ala Thr Lys Lys Asn Val Thr Gly Thr His Arg Ser Ser Ser Ser Ser
 405 410 415

Ser Pro Ser Ala Ser Ser Asn Ala Ala Val Ser Ala Val Ala Pro Ala
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Ala Gly Val Ser Gly Leu Leu Leu Gly Leu Ala Leu Asn Leu Leu
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<210> 22

<211> 8

<212> PRT

<213> Mycobacterium tuberculosis

<400> 22

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PCT/CA2003/001554

Asn Asp Met His Asp Gly Ser Ile
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